Jarrell, Noble 178582

From: Ramirez, Delia
Sent: Friday, February 03, 2006 2:32 PM
To: Jarrell, Noble
Subject: 10/675685

Hi,

I would like to request the following alignments:

1. SEQ ID NO: 3 against SEQ ID NO:7, 10 and 16
2. SEQ ID NO: 7 against SEQ ID NO:14 and 18

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

Noble
Fax 2/3/06
10 PR 4AA
10 ONL gcg

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 3, 2006, 15:17:20 ; Search time 0.001 Seconds
(without alignments)
0.684 Million cell updates/sec

Title: US-10-675-685-14
Perfect score: 178
Sequence: 1 VISQLLLLVPPLSQQEHTYATYLQSKIVALPSRWLV 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 19 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : Pending_Patents_AA_Main:US-10-675-685-7
1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:US-10-675-685-7
2: /cgn2_6/ptodata/1/paa/US066_COMB.pep:US-10-675-685-7
3: /cgn2_6/ptodata/1/paa/US073_COMB.pep:US-10-675-685-7
4: /cgn2_6/ptodata/1/paa/US074_COMB.pep:US-10-675-685-7
5: /cgn2_6/ptodata/1/paa/US075_COMB.pep:US-10-675-685-7
6: /cgn2_6/ptodata/1/paa/US076_COMB.pep:US-10-675-685-7
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16: /cgn2_6/ptodata/1/paa/US086_COMB.pep:US-10-675-685-7
17: /cgn2_6/ptodata/1/paa/US087_COMB.pep:US-10-675-685-7
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20: /cgn2_6/ptodata/1/paa/US090_COMB.pep:US-10-675-685-7
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25: /cgn2_6/ptodata/1/paa/US095_COMB.pep:US-10-675-685-7
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31: /cgn2_6/ptodata/1/paa/US101_COMB.pep:US-10-675-685-7
32: /cgn2_6/ptodata/1/paa/US102_COMB.pep:US-10-675-685-7
33: /cgn2_6/ptodata/1/paa/US103_COMB.pep:US-10-675-685-7
34: /cgn2_6/ptodata/1/paa/US104_COMB.pep:US-10-675-685-7
35: /cgn2_6/ptodata/1/paa/US105_COMB.pep:US-10-675-685-7
36: /cgn2_6/ptodata/1/paa/US106_COMB.pep:US-10-675-685-7
37: /cgn2_6/ptodata/1/paa/US107_COMB.pep:US-10-675-685-7
38: /cgn2_6/ptodata/1/paa/US108_COMB.pep:US-10-675-685-7
39: /cgn2_6/ptodata/1/paa/US109_COMB.pep:US-10-675-685-7
40: /cgn2_6/ptodata/1/paa/US110_COMB.pep:US-10-675-685-7
41: /cgn2_6/ptodata/1/paa/US111_COMB.pep:US-10-675-685-7
42: /cgn2_6/ptodata/1/paa/US112_COMB.pep:US-10-675-685-7
43: /cgn2_6/ptodata/1/paa/US114_COMB.pep:US-10-675-685-7
44: /cgn2_6/ptodata/1/paa/US600_COMB.pep:US-10-675-685-7
45: /cgn2_6/ptodata/1/paa/US601_COMB.pep:US-10-675-685-7
46: /cgn2_6/ptodata/1/paa/US602_COMB.pep:US-10-675-685-7
47: /cgn2_6/ptodata/1/paa/US603_COMB.pep:US-10-675-685-7
48: /cgn2_6/ptodata/1/paa/US604_COMB.pep:US-10-675-685-7
49: /cgn2_6/ptodata/1/paa/US605_COMB.pep:US-10-675-685-7
50: /cgn2_6/ptodata/1/paa/US606_COMB.pep:US-10-675-685-7
51: /cgn2_6/ptodata/1/paa/US607_COMB.pep:US-10-675-685-7

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14	7.9	19	36	US-10-675-685-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-675-685-7
; Sequence 7, Application US/10675685
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-675-685-7

Query Match 7.9%; Score 14; DB 36; Length 19;
Best Local Similarity 28.6%; Pred. No. 0;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Qy         28 VALPSRW 34
              :|: : |
Db         11 LAILAGW 17
```

Search completed: February 3, 2006, 15:17:20
Job time : 0.001 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 3, 2006, 15:17:20 ; Search time 0.001 Seconds
(without alignments)
0.380 Million cell updates/sec

Title: US-10-675-685-18
Perfect score: 105
Sequence: 1 GQNNPAIIAGGIVLSPAYYG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 19 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : Pending_Patents_AA_Main:US-10-675-685-7
1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:US-10-675-685-7
2: /cgn2_6/ptodata/1/paa/US066_COMB.pep:US-10-675-685-7
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4: /cgn2_6/ptodata/1/paa/US074_COMB.pep:US-10-675-685-7
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46: /cgn2_6/ptodata/1/paa/US602_COMB.pep:US-10-675-685-7
47: /cgn2_6/ptodata/1/paa/US603_COMB.pep:US-10-675-685-7
48: /cgn2_6/ptodata/1/paa/US604_COMB.pep:US-10-675-685-7
49: /cgn2_6/ptodata/1/paa/US605_COMB.pep:US-10-675-685-7
50: /cgn2_6/ptodata/1/paa/US606_COMB.pep:US-10-675-685-7
51: /cgn2_6/ptodata/1/paa/US607_COMB.pep:US-10-675-685-7

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query	No.	Score	Match Length	DB	ID	Description
		1	20	19.0 19	36	US-10-675-685-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-675-685-7
; Sequence 7, Application US/10675685
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-675-685-7

Query Match 19.0%; Score 20; DB 36; Length 19;
Best Local Similarity 80.0%; Pred. No. 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 AIIAG 10
              ||:||
Db         12 AILAG 16
```

Search completed: February 3, 2006, 15:17:21
Job time : 1 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 3, 2006, 15:09:35 ; Search time 1 Seconds
(without alignments)
5.685 Million cell updates/sec

Title: US-10-675-685-3
Perfect score: 9858
Sequence: 1 MMCLKILRISLAILAGWALC.....AADCDLDECTCRDPKAEENQ 1791

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3 seqs, 3174 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database : US10675685.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9524	96.6	1770	1	US-10-675-685-10	Sequence 10, Appl
2	7351	74.6	1385	1	US-10-675-685-16	Sequence 16, Appl
3	94	1.0	19	1	US-10-675-685-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-675-685-10
; Sequence 10, Application US/10675685
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10
; LENGTH: 1770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-675-685-10

Query Match 96.6%; Score 9524; DB 1; Length 1770;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MMCLKILRISLAILAGWALCSANSELGWTRKKSLVEREHLNQVLLEGERCWLGAKVRRPR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMCLKILRISLAILAGWALCSANSELGWTRKKSLVEREHLNQVLLEGERCWLGAKVRRPR 60

Qy         61 ASPQHHLFGVYPSRAGNYLRPYPVGEQEIHHTGRSKPDTEGNAVSLVPPDLTENPAGLRG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ASPQHHLFGVYPSRAGNYLRPYPVGEQEIHHTGRSKPDTEGNAVSLVPPDLTENPAGLRG 120

Qy        121 AVEEPAAPWVGDSPIGQSELLGDDDAYLGNQRSKESLGEAGIQKGSAMAATTTTAIFTTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AVEEPAAPWVGDSPIGQSELLGDDDAYLGNQRSKESLGEAGIQKGSAMAATTTTAIFTTL 180

Qy        181 NEPKPETQRRGWAKSRQRRQVWKRRAEDGQGDSGISSHFQPWPKHSLKHRVKKSPPEESN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NEPKPETQRRGWAKSRQRRQVWKRRAEDGQGDSGISSHFQPWPKHSLKHRVKKSPPEESN 240

Qy        241 QNGGEGSYREAETFNSQVGLPILYFSGRRERLLLRPEVLAEIPREAFTVEAWVKPEGGQN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 QNGGEGSYREAETFNSQVGLPILYFSGRRERLLLRPEVLAEIPREAFTVEAWVKPEGGQN 300

Qy        301 NPAIIAGVFDNCSHTVSDKGWALGIRSGKDKGKRDARFFFSLCTDRVKKATILISHSRYQ 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPAIIAGVFDNCSHTVSDKGWALGIRSGKDKGKRDARFFFSLCTDRVKKATILISHSRYQ 360

Qy        361 PGTWTHVAATYDGRHMALYVDGTQVASSLDQSGPLNSPFMASCRSLLLGGDSSEDGHYFR 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PGTWTHVAATYDGRHMALYVDGTQVASSLDQSGPLNSPFMASCRSLLLGGDSSEDGHYFR 420

Qy        421 GHLGTLVFWSTALPQSHFQHSSQHSSEEEEATDLVLTASFEPVNTEWVPFRDEKYPRLEV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GHLGTLVFWSTALPQSHFQHSSQHSSEEEEATDLVLTASFEPVNTEWVPFRDEKYPRLEV 480

Qy        481 LQGFEPEPEILSPLQPPLCGQTVCDNVELISQYNGYWPLRGEKVIRYQVVNICDDEGLNP 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LQGFEPEPEILSPLQPPLCGQTVCDNVELISQYNGYWPLRGEKVIRYQVVNICDDEGLNP 540

Qy        541 IVSEEQIRLQHEALNEAFSRYNISWQLSVHQVHNSTLRHRVVLVNCEPSKIGNDHCDPEC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 IVSEEQIRLQHEALNEAFSRYNISWQLSVHQVHNSTLRHRVVLVNCEPSKIGNDHCDPEC 600

Qy        601 EHPLTGYDGGDCRLQGRCYSWNRRDGLCHVECNNMLNDFDDGDCCDPQVADVRKTCFDPD 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 EHPLTGYDGGDCRLQGRCYSWNRRDGLCHVECNNMLNDFDDGDCCDPQVADVRKTCFDPD 660

Qy        661 SPKRAYMSVKELKEALQLNSTHFLNIYFASSVREDLAGAATWPWDKDAVTHLGGIVLSPA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SPKRAYMSVKELKEALQLNSTHFLNIYFASSVREDLAGAATWPWDKDAVTHLGGIVLSPA 720

Qy        721 YYGMPGHTDTMIHEVGHVLGLYHVFKGVSERESCNDPCKETVPSMETGDLCADTAPTPKS 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 YYGMPGHTDTMIHEVGHVLGLYHVFKGVSERESCNDPCKETVPSMETGDLCADTAPTPKS 780

Qy        781 ELCREPEPTSDTCGFTRFPGAPFTNYMSYTDDNCTDNFTPNQVARMHCYLDLVYQQWTES 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ELCREPEPTSDTCGFTRFPGAPFTNYMSYTDDNCTDNFTPNQVARMHCYLDLVYQQWTES 840

Qy        841 RKPTPIPIPPMVIGQTNKSLTIHWLPPISGVVYDRASGSLCGACTEDGTFRQYVHTASSR 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RKPTPIPIPPMVIGQTNKSLTIHWLPPISGVVYDRASGSLCGACTEDGTFRQYVHTASSR 900

Qy        901 RVCDSSGYWTPEEAVGPPDVDQPCEPSLQAWSPEVHLYHMNMTVPCPTEGCSLELLFQHP 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RVCDSSGYWTPEEAVGPPDVDQPCEPSLQAWSPEVHLYHMNMTVPCPTEGCSLELLFQHP 960

Qy        961 VQADTLTLWVTSFFMESSQVLFDTEILLENKESVHLGPLDTFCDIPLTIKLHVDGKVSGV 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 VQADTLTLWVTSFFMESSQVLFDTEILLENKESVHLGPLDTFCDIPLTIKLHVDGKVSGV 1020

Qy       1021 KVYTFDERIEIDAALLTSQPHSPLCSGCRPVRYQVLRDPPFASGLPVVVTHSHRKFTDVE 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 KVYTFDERIEIDAALLTSQPHSPLCSGCRPVRYQVLRDPPFASGLPVVVTHSHRKFTDVE 1080
```

```
Qy       1081 VTPGQMYQYQVLAEAGGELGEASPPLNHIHGAPYCGDGKVSERLGEECDDGDLVSGDGCS 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 VTPGQMYQYQVLAEAGGELGEASPPLNHIHGAPYCGDGKVSERLGEECDDGDLVSGDGCS 1140

Qy       1141 KVCELEEGFNCVGEPSLCYMYEGDGICEPFERKTSIVDCGIYTPKGYLDQWATRAYSSHE 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 KVCELEEGFNCVGEPSLCYMYEGDGICEPFERKTSIVDCGIYTPKGYLDQWATRAYSSHE 1200

Qy       1201 DKKKCPVSLVTGEPHSLICTSYHPDLPNHRPLTGWFPCVASENETQDDRSEQPEGSLKKE 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 DKKKCPVSLVTGEPHSLICTSYHPDLPNHRPLTGWFPCVASENETQDDRSEQPEGSLKKE 1260

Qy       1261 DEVWLKVCFNRPGEARAIFIFLTTDGLVPGEHQQPTVTLYLTDVRGSNHSLGTYGLSCQH 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 DEVWLKVCFNRPGEARAIFIFLTTDGLVPGEHQQPTVTLYLTDVRGSNHSLGTYGLSCQH 1320

Qy       1321 NPLIINVTHHQNVLFHHTTSVLPNFSSPRVGISAVALRTSSRIGLSAPSNCISEDEGQNH 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 NPLIINVTHHQNVLFHHTTSVLPNFSSPRVGISAVALRTSSRIGLSAPSNCISEDEGQNH 1380

Qy       1381 QGQSCIHRPCGKQDSCPSLLLDHADVVNCTSIGPGLMKCAITCQRGFALQASSGQYIRPM 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 QGQSCIHRPCGKQDSCPSLLLDHADVVNCTSIGPGLMKCAITCQRGFALQASSGQYIRPM 1440

Qy       1441 QKEILLTCSSGHWDQNVSCLPVDCGVPDPSLVNYANFSCSEGTKFLKRCSISCVPPAKLQ 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 QKEILLTCSSGHWDQNVSCLPVDCGVPDPSLVNYANFSCSEGTKFLKRCSISCVPPAKLQ 1500

Qy       1501 GLSPWLTCLEDGLWSLPEVYCKLECDAPPIILNANLLLPHCLQDNHDVGTICKYECKPGY 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GLSPWLTCLEDGLWSLPEVYCKLECDAPPIILNANLLLPHCLQDNHDVGTICKYECKPGY 1560

Qy       1561 YVAESAEGKVRNKLLKIQCLEGGIWEQGSCIPVVCEPPPPVFEGMYECTNGFSLDSQCVL 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 YVAESAEGKVRNKLLKIQCLEGGIWEQGSCIPVVCEPPPPVFEGMYECTNGFSLDSQCVL 1620

Qy       1621 NCNQEREKLPILCTKEGLWTQEFKLCENLQGECPPPPSELNSVEYKCEQGYGIGAVCSPL 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 NCNQEREKLPILCTKEGLWTQEFKLCENLQGECPPPPSELNSVEYKCEQGYGIGAVCSPL 1680

Qy       1681 CVIPPSDPVMLPENITADTLEHWMEPVKVQSIVCTGRRQWHPDPVLVHCIQSCE 1734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CVIPPSDPVMLPENITADTLEHWMEPVKVQSIVCTGRRQWHPDPVLVHCIQSCE 1734
```

RESULT 2
US-10-675-685-16
; Sequence 16, Application US/10675685
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE:. 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 16
; LENGTH: 1385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-675-685-16

Query Match 74.6%; Score 7351; DB 1; Length 1385;
Best Local Similarity 76.9%; Pred. No. 0;
Matches 1377; Conservative 1; Mismatches 7; Indels 406; Gaps 1;

```
Qy          1 MMCLKILRISLAILAGWALCSANSELGWTRKKSLVEREHLNQVLLEGERCWLGAKVRRPR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMCLKILRISLAILAGWALCSANSELGWTRKKSLVEREHLNQVLLEGERCWLGAKVRRPR 60

Qy         61 ASPQHHLFGVYPSRAGNYLRPYPVGEQEIHHTGRSKPDTEGNAVSLVPPDLTENPAGLRG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ASPQHHLFGVYPSRAGNYLRPYPVGEQEIHHTGRSKPDTEGNAVSLVPPDLTENPAGLRG 120

Qy        121 AVEEPAAPWVGDSPIGQSELLGDDDAYLGNQRSKESLGEAGIQKGSAMAATTTTAIFTTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AVEEPAAPWVGDSPIGQSELLGDDDAYLGNQRSKESLGEAGIQKGSAMAATTTTAIFTTL 180

Qy        181 NEPKPETQRRGWAKSRQRRQVWKRRAEDGQGDSGISSHFQPWPKHSLKHRVKKSPPEESN 240
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        181 NEPKPETQRRGWAKSRQRRQVWKRRAEDGQGDSGISSHFQPWPKHSLKHGVKKSPPEESN 240

Qy        241 QNGGEGSYREAETFNSQVGLPILYFSGRRERLLLRPEVLAEIPREAFTVEAWVKPEGGQN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 QNGGEGSYREAETFNSQVGLPILYFSGRRERLLLRPEVLAEIPREAFTVEAWVKPEGGQN 300

Qy        301 NPAIIAGVFDNCSHTVSDKGWALGIRSGKDKGKRDARFFFSLCTDRVKKATILISHSRYQ 360
              ||||||
Db        301 NPAIIA---------------------------------------------------- 306

Qy        361 PGTWTHVAATYDGRHMALYVDGTQVASSLDQSGPLNSPFMASCRSLLLGGDSSEDGHYFR 420

Db        307 ---------------------------------------------------------- 306

Qy        421 GHLGTLVFWSTALPQSHFQHSSQHSSEEEEATDLVLTASFEPVNTEWVPFRDEKYPRLEV 480

Db        307 ---------------------------------------------------------- 306

Qy        481 LQGFEPEPEILSPLQPPLCGQTVCDNVELISQYNGYWPLRGEKVIRYQVVNICDDEGLNP 540

Db        307 ---------------------------------------------------------- 306

Qy        541 IVSEEQIRLQHEALNEAFSRYNISWQLSVHQVHNSTLRHRVVLVNCEPSKIGNDHCDPEC 600

Db        307 ---------------------------------------------------------- 306

Qy        601 EHPLTGYDGGDCRLQGRCYSWNRRDGLCHVECNNMLNDFDDGDCCDPQVADVRKTCFDPD 660

Db        307 ---------------------------------------------------------- 306

Qy        661 SPKRAYMSVKELKEALQLNSTHFLNIYFASSVREDLAGAATWPWDKDAVTHLGGIVLSPA 720
                                                                ||||||||
Db        307 ----------------------------------------------------GGIVLSPA 314

Qy        721 YYGMPGHTDTMIHEVGHVLGLYHVFKGVSERESCNDPCKETVPSMETGDLCADTAPTPKS 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 YYGMPGHTDTMIHEVGHVLGLYHVFKGVSERESCNDPCKETVPSMETGDLCADTAPTPKS 374

Qy        781 ELCREPEPTSDTCGFTRFPGAPFTNYMSYTDDNCTDNFTPNQVARMHCYLDLVYQQWTES 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 ELCREPEPTSDTCGFTRFPGAPFTNYMSYTDDNCTDNFTPNQVARMHCYLDLVYQQWTES 434

Qy        841 RKPTPIPIPPMVIGQTNKSLTIHWLPPISGVVYDRASGSLCGACTEDGTFRQYVHTASSR 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 RKPTPIPIPPMVIGQTNKSLTIHWLPPISGVVYDRASGSLCGACTEDGTFRQYVHTASSR 494

Qy        901 RVCDSSGYWTPEEAVGPPDVDQPCEPSLQAWSPEVHLYHMNMTVPCPTEGCSLELLFQHP 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 RVCDSSGYWTPEEAVGPPDVDQPCEPSLQAWSPEVHLYHMNMTVPCPTEGCSLELLFQHP 554

Qy        961 VQADTLTLWVTSFFMESSQVLFDTEILLENKESVHLGPLDTFCDIPLTIKLHVDGKVSGV 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 VQADTLTLWVTSFFMESSQVLFDTEILLENKESVHLGPLDTFCDIPLTIKLHVDGKVSGV 614

Qy       1021 KVYTFDERIEIDAALLTSQPHSPLCSGCRPVRYQVLRDPPPASGLPVVVTHSHRKFTDVE 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        615 KVYTFDERIEIDAALLTSQPHSPLCSGCRPVRYQVLRDPPPASGLPVVVTHSHRKFTDVE 674

Qy       1081 VTPGQMYQYQVLAEAGGELGEASPPLNHIHGAPYCGDGKVSERLGEECDDGDLVSGDGCS 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        675 VTPGQMYQYQVLAEAGGELGEASPPLNHIHGAPYCGDGKVSERLGEECDDGDLVSGDGCS 734
```

```
Qy       1141 KVCELEEGFNCVGEPSLCYMYEGDGICEPPERKTSIVDCGIYTPKGYLDQWATRAYSSHE 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        735 KVCELEEGFNCVGEPSLCYMYEGDGICEPPERKTSIVDCGIYTPKGYLDQWATRAYSSHE 794

Qy       1201 DKKKCPVSLVTGEPHSLICTSYHPDLPNHRPLTGWFPCVASENETQDDRSEQPEGSLKKE 1260
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        795 DKKKCPVSLVTGEPHSLIRTSYHPDLPNHRPLTGWFPCVASENETQDDRSEQPEGSLKKE 854

Qy       1261 DEVWLKVCFNRPGEARAIFIFLTTDGLVPGEHQQPTVTLYLTDVRGSNHSLGTYGLSCQH 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        855 DEVWLKVCFNRPGEARAIFIFLTTDGLVPGEHQQPTVTLYLTDVRGSNHSLGTYGLSCQH 914

Qy       1321 NPLIINVTHHQNVLFHHTTSVLPNFSSPRVGISAVALRTSSRIGLSAPSNCISEDEGQNH 1380
             ||||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||||
Db        915 NPLIINVTHHQNVLFRHTTSVLLNFSSPRVGISAVALRTSSRIGLSAPSNCISEDEGQNH 974

Qy       1381 QGQSCIHRPCGKQDSCPSLLLDHADVVNCTSIGPGLMKCAITCQRGFALQASSGQYIRPM 1440
             |||||||||||||||||||||||||||||||||||| |||||||||||| |||| |
Db        975 QGQSCIHRPCGKQDSCPSLLLDHADVVNCTSIGPGLMKCATTCQRGFALQASSEQYIRLM 1034

Qy       1441 QKEILLTCSSGHWDQNVSCLPVDCGVPDPSLVNYANFSCSEGTKFLKRCSISCVPPAKLQ 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1035 QKEILLTCSSGHWDQNVSCLPVDCGVPDPSLVNYANFSCSEGTKFLKRCSISCVPPAKLQ 1094

Qy       1501 GLSPWLTCLEDGLWSLPEVYCKLECDAPPIILNANLLLPHCLQDNHDVGTICKYECKPGY 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1095 GLSPWLTCLEDGLWSLPEVYCKLECDAPPIILNANLLLPHCLQDNHDVGTICKYECKPGY 1154

Qy       1561 YVAESAEGKVRNKLLKIQCLEGGIWEQGSCIPVVCEPPPPVFEGMYECTNGFSLDSQCVL 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1155 YVAESAEGKVRNKLLKIQCLEGGIWEQGSCIPVVCEPPPPVFEGMYECTNGFSLDSQCVL 1214

Qy       1621 NCNQEREKLPILCTKEGLWTQEFKLCENLQGECPPPPSELNSVEYKCEQGYGIGAVCSPL 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1215 NCNQEREKLPILCTKEGLWTQEFKLCENLQGECPPPPSELNSVEYKCEQGYGIGAVCSPL 1274

Qy       1681 CVIPPSDPVMLPENITADTLEHWMEPVKVQSIVCTGRRQWHPDPVLVHCIQSCEPFQANG 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db       1275 CVIPPSDPVMLPENITADTLEHWMEPVKVQSIVCTGRRQWHPDPVLVHCIQSCEPFQADG 1334

Qy       1741 WCDTINNRAYCHYDGGDCCSSTLSSKKVIPFAADCDLDECTCRDPKAEENQ 1791
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1335 WCDTINNRAYCHYDGGDCCSSTLSSKKVIPFAADCDLDECTCRDPKAEENQ 1385
```

RESULT 3
US-10-675-685-7
; Sequence 7, Application US/10675685
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-675-685-7

Query Match 1.0%; Score 94; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MMCLKILRISLAILAGWAL 19
              |||||||||||||||||||
Db          1 MMCLKILRISLAILAGWAL 19
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Search completed: February 3, 2006, 15:09:43
Job time : 4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2006, 15:10:59 ; Search time 0.0119723 Seconds
(without alignments)
2.842 Million cell updates/sec

Title: US-10-675-685-7
Perfect score: 94
Sequence: 1 MMCLKILRISLAILAGWAL 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1791 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : Pending_Patents_AA_Main:US-10-675-685-3
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2: /cgn2_6/ptodata/1/paa/US066_COMB.pep:US-10-675-685-3
3: /cgn2_6/ptodata/1/paa/US073_COMB.pep:US-10-675-685-3
4: /cgn2_6/ptodata/1/paa/US074_COMB.pep:US-10-675-685-3
5: /cgn2_6/ptodata/1/paa/US075_COMB.pep:US-10-675-685-3
6: /cgn2_6/ptodata/1/paa/US076_COMB.pep:US-10-675-685-3
7: /cgn2_6/ptodata/1/paa/US077_COMB.pep:US-10-675-685-3
8: /cgn2_6/ptodata/1/paa/US078_COMB.pep:US-10-675-685-3
9: /cgn2_6/ptodata/1/paa/US079_COMB.pep:US-10-675-685-3
10: /cgn2_6/ptodata/1/paa/US080_COMB.pep:US-10-675-685-3
11: /cgn2_6/ptodata/1/paa/US081_COMB.pep:US-10-675-685-3
12: /cgn2_6/ptodata/1/paa/US082_COMB.pep:US-10-675-685-3
13: /cgn2_6/ptodata/1/paa/US083_COMB.pep:US-10-675-685-3
14: /cgn2_6/ptodata/1/paa/US084_COMB.pep:US-10-675-685-3
15: /cgn2_6/ptodata/1/paa/US085_COMB.pep:US-10-675-685-3
16: /cgn2_6/ptodata/1/paa/US086_COMB.pep:US-10-675-685-3
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24: /cgn2_6/ptodata/1/paa/US094_COMB.pep:US-10-675-685-3
25: /cgn2_6/ptodata/1/paa/US095_COMB.pep:US-10-675-685-3
26: /cgn2_6/ptodata/1/paa/US096_COMB.pep:US-10-675-685-3
27: /cgn2_6/ptodata/1/paa/US097_COMB.pep:US-10-675-685-3
28: /cgn2_6/ptodata/1/paa/US098_COMB.pep:US-10-675-685-3
29: /cgn2_6/ptodata/1/paa/US099_COMB.pep:US-10-675-685-3
30: /cgn2_6/ptodata/1/paa/US100_COMB.pep:US-10-675-685-3
31: /cgn2_6/ptodata/1/paa/US101_COMB.pep:US-10-675-685-3
32: /cgn2_6/ptodata/1/paa/US102_COMB.pep:US-10-675-685-3
33: /cgn2_6/ptodata/1/paa/US103_COMB.pep:US-10-675-685-3
34: /cgn2_6/ptodata/1/paa/US104_COMB.pep:US-10-675-685-3
35: /cgn2_6/ptodata/1/paa/US105_COMB.pep:US-10-675-685-3
36: /cgn2_6/ptodata/1/paa/US106_COMB.pep:US-10-675-685-3
37: /cgn2_6/ptodata/1/paa/US107_COMB.pep:US-10-675-685-3
38: /cgn2_6/ptodata/1/paa/US108_COMB.pep:US-10-675-685-3
39: /cgn2_6/ptodata/1/paa/US109_COMB.pep:US-10-675-685-3
40: /cgn2_6/ptodata/1/paa/US110_COMB.pep:US-10-675-685-3
41: /cgn2_6/ptodata/1/paa/US111_COMB.pep:US-10-675-685-3
42: /cgn2_6/ptodata/1/paa/US112_COMB.pep:US-10-675-685-3
43: /cgn2_6/ptodata/1/paa/US114_COMB.pep:US-10-675-685-3
44: /cgn2_6/ptodata/1/paa/US600_COMB.pep:US-10-675-685-3
45: /cgn2_6/ptodata/1/paa/US601_COMB.pep:US-10-675-685-3
46: /cgn2_6/ptodata/1/paa/US602_COMB.pep:US-10-675-685-3
47: /cgn2_6/ptodata/1/paa/US603_COMB.pep:US-10-675-685-3
48: /cgn2_6/ptodata/1/paa/US604_COMB.pep:US-10-675-685-3
49: /cgn2_6/ptodata/1/paa/US605_COMB.pep:US-10-675-685-3
50: /cgn2_6/ptodata/1/paa/US606_COMB.pep:US-10-675-685-3
51: /cgn2_6/ptodata/1/paa/US607_COMB.pep:US-10-675-685-3

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	94	100.0	1791	36	US-10-675-685-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-675-685-3
; Sequence 3, Application US/10675685
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3
; LENGTH: 1791
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-675-685-3

Query Match 100.0%; Score 94; DB 36; Length 1791;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MMCLKILRISLAILAGWAL 19
              |||||||||||||||||||
Db          1 MMCLKILRISLAILAGWAL 19
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Search completed: February 3, 2006, 15:11:01
Job time : 0.0119723 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2006, 15:10:59 ; Search time 1.11531 Seconds
(without alignments)
2.842 Million cell updates/sec

Title: US-10-675-685-10
Perfect score: 9702
Sequence: 1 MMCLKILRISLAILAGWALC.....HTYATYLQSKIVALPSRWLV 1770

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1791 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : Pending_Patents_AA_Main:US-10-675-685-3
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50: /cgn2_6/ptodata/1/paa/US606_COMB.pep:US-10-675-685-3
51: /cgn2_6/ptodata/1/paa/US607_COMB.pep:US-10-675-685-3

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query	No.	Score	Match Length	DB	ID	Description
		1	9524	98.2 1791	36	US-10-675-685-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-675-685-3
; Sequence 3, Application US/10675685
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3
; LENGTH: 1791
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-675-685-3

Query Match 98.2%; Score 9524; DB 36; Length 1791;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MMCLKILRISLAILAGWALCSANSELGWTRKKSLVEREHLNQVLLEGERCWLGAKVRRPR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMCLKILRISLAILAGWALCSANSELGWTRKKSLVEREHLNQVLLEGERCWLGAKVRRPR 60

Qy         61 ASPQHHLFGVYPSRAGNYLRPYPVGEQEIHHTGRSKPDTEGNAVSLVPPDLTENPAGLRG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ASPQHHLFGVYPSRAGNYLRPYPVGEQEIHHTGRSKPDTEGNAVSLVPPDLTENPAGLRG 120

Qy        121 AVEEPAAPWVGDSPIGQSELLGDDDAYLGNQRSKESLGEAGIQKGSAMAATTTTAIFTTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AVEEPAAPWVGDSPIGQSELLGDDDAYLGNQRSKESLGEAGIQKGSAMAATTTTAIFTTL 180

Qy        181 NEPKPETQRRGWAKSRQRRQVWKRRAEDGQGDSGISSHFQPWPKHSLKHRVKKSPPEESN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 QNGGEGSYREAETFNSQVGLPILYFSGRRERLLLRPEVLAEIPREAFTVEAWVKPEGGQN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 QNGGEGSYREAETFNSQVGLPILYFSGRRERLLLRPEVLAEIPREAFTVEAWVKPEGGQN 300

Qy        301 NPAIIAGVFDNCSHTVSDKGWALGIRSGKDKGKRDARFFFSLCTDRVKKATILISHSRYQ 360
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Db        301 NPAIIAGVFDNCSHTVSDKGWALGIRSGKDKGKRDARFFFSLCTDRVKKATILISHSRYQ 360

Qy        361 PGTWTHVAATYDGRHMALYVDGTQVASSLDQSGPLNSPFMASCRSLLLGGDSSEDGHYFR 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PGTWTHVAATYDGRHMALYVDGTQVASSLDQSGPLNSPFMASCRSLLLGGDSSEDGHYFR 420

Qy        421 GHLGTLVFWSTALPQSHFQHSSQHSSEEEEATDLVLTASFEPVNTEWVPFRDEKYPRLEV 480
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Db        421 GHLGTLVFWSTALPQSHFQHSSQHSSEEEEATDLVLTASFEPVNTEWVPFRDEKYPRLEV 480

Qy        481 LQGFEPEPEILSPLQPPLCGQTVCDNVELISQYNGYWPLRGEKVIRYQVVNICDDEGLNP 540
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Db        481 LQGFEPEPEILSPLQPPLCGQTVCDNVELISQYNGYWPLRGEKVIRYQVVNICDDEGLNP 540

Qy        541 IVSEEQIRLQHEALNEAFSRYNISWQLSVHQVHNSTLRHRVVLVNCEPSKIGNDHCDPEC 600
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Db        541 IVSEEQIRLQHEALNEAFSRYNISWQLSVHQVHNSTLRHRVVLVNCEPSKIGNDHCDPEC 600
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Qy       601 EHPLTGYDGGDCRLQGRCYSWNRRDGLCHVECNNMLNDFDDGDCCDPQVADVRKTCFDPD 660
Db       601 EHPLTGYDGGDCRLQGRCYSWNRRDGLCHVECNNMLNDFDDGDCCDPQVADVRKTCFDPD 660

Qy       661 SPKRAYMSVKELKEALQLNSTHFLNIYFASSVREDLAGAATWPWDKDAVTHLGGIVLSPA 720
Db       661 SPKRAYMSVKELKEALQLNSTHFLNIYFASSVREDLAGAATWPWDKDAVTHLGGIVLSPA 720

Qy       721 YYGMPGHTDTMIHEVGHVLGLYHVFKGVSERESCNDPCKETVPSMETGDLCADTAPTPKS 780
Db       721 YYGMPGHTDTMIHEVGHVLGLYHVFKGVSERESCNDPCKETVPSMETGDLCADTAPTPKS 780

Qy       781 ELCREPEPTSDTCGFTRFPGAPFTNYMSYTDDNCTDNFTPNQVARMHCYLDLVYQQWTES 840
Db       781 ELCREPEPTSDTCGFTRFPGAPFTNYMSYTDDNCTDNFTPNQVARMHCYLDLVYQQWTES 840

Qy       841 RKPTPIPIPPMVIGQTNKSLTIHWLPPISGVVYDRASGSLCGACTEDGTFRQYVHTASSR 900
Db       841 RKPTPIPIPPMVIGQTNKSLTIHWLPPISGVVYDRASGSLCGACTEDGTFRQYVHTASSR 900

Qy       901 RVCDSSGYWTPEEAVGPPDVDQPCEPSLQAWSPEVHLYHMNMTVPCPTEGCSLELLFQHP 960
Db       901 RVCDSSGYWTPEEAVGPPDVDQPCEPSLQAWSPEVHLYHMNMTVPCPTEGCSLELLFQHP 960

Qy       961 VQADTLTLWVTSFFMESSQVLFDTEILLENKESVHLGPLDTFCDIPLTIKLHVDGKVSGV 1020
Db       961 VQADTLTLWVTSFFMESSQVLFDTEILLENKESVHLGPLDTFCDIPLTIKLHVDGKVSGV 1020

Qy      1021 KVYTFDERIEIDAALLTSQPHSPLCSGCRPVRYQVLRDPPFASGLPVVVTHSHRKFTDVE 1080
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Qy      1081 VTPGQMYQYQVLAEAGGELGEASPPLNHIHGAPYCGDGKVSERLGEECDDGDLVSGDGCS 1140
Db      1081 VTPGQMYQYQVLAEAGGELGEASPPLNHIHGAPYCGDGKVSERLGEECDDGDLVSGDGCS 1140

Qy      1141 KVCELEEGFNCVGEPSLCYMYEGDGICEPFERKTSIVDCGIYTPKGYLDQWATRAYSSHE 1200
Db      1141 KVCELEEGFNCVGEPSLCYMYEGDGICEPFERKTSIVDCGIYTPKGYLDQWATRAYSSHE 1200

Qy      1201 DKKKCPVSLVTGEPHSLICTSYHPDLPNHRPLTGWFPCVASENETQDDRSEQPEGSLKKE 1260
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Qy      1261 DEVWLKVCFNRPGEARAIFIFLTTDGLVPGEHQQPTVTLYLTDVRGSNHSLGTYGLSCQH 1320
Db      1261 DEVWLKVCFNRPGEARAIFIFLTTDGLVPGEHQQPTVTLYLTDVRGSNHSLGTYGLSCQH 1320

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Db      1321 NPLIINVTHHQNVLFHHTTSVLPNFSSPRVGISAVALRTSSRIGLSAPSNCISEDEGQNH 1380

Qy      1381 QGQSCIHRPCGKQDSCPSLLLDHADVVNCTSIGPGLMKCAITCQRGFALQASSGQYIRPM 1440
Db      1381 QGQSCIHRPCGKQDSCPSLLLDHADVVNCTSIGPGLMKCAITCQRGFALQASSGQYIRPM 1440

Qy      1441 QKEILLTCSSGHWDQNVSCLPVDCGVPDPSLVNYANFSCSEGTKFLKRCSISCVPPAKLQ 1500
Db      1441 QKEILLTCSSGHWDQNVSCLPVDCGVPDPSLVNYANFSCSEGTKFLKRCSISCVPPAKLQ 1500

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Db      1501 GLSPWLTCLEDGLWSLPEVYCKLECDAPPIILNANLLLPHCLQDNHDVGTICKYECKPGY 1560

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Search completed: February 3, 2006, 15:11:01
Job time : 1.11531 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 3, 2006, 15:10:59 ; Search time 0.872716 Seconds
(without alignments)
2.842 Million cell updates/sec

Title: US-10-675-685-16
Perfect score: 7617
Sequence: 1 MMCLKILRISLAILAGWALC.....AADCDLDECTCRDPKAEENQ 1385

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1791 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

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              51:  /cgn2_6/ptodata/1/paa/US607_COMB.pep:US-10-675-685-3

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                  SUMMARIES

                      %
Result                Query
  No.    Score        Match Length DB  ID                          Description
-------------------------------------------------------------------------------
    1     7351         96.5   1791  36  US-10-675-685-3             Sequence 3, Appli

                                 ALIGNMENTS


RESULT 1
US-10-675-685-3
; Sequence 3, Application US/10675685
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: PB0114
;  CURRENT APPLICATION NUMBER: US/10/675,685
;  CURRENT FILING DATE:  2003-09-30
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3
;   LENGTH: 1791
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-675-685-3

  Query Match             96.5%;  Score 7351;  DB 36;  Length 1791;
  Best Local Similarity   76.9%;  Pred. No. 0;
  Matches 1377;  Conservative    1;  Mismatches    7;  Indels  406;  Gaps    1;

Qy          1 MMCLKILRISLAILAGWALCSANSELGWTRKKSLVEREHLNQVLLEGERCWLGAKVRRPR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMCLKILRISLAILAGWALCSANSELGWTRKKSLVEREHLNQVLLEGERCWLGAKVRRPR 60

Qy         61 ASPQHHLFGVYPSRAGNYLRPYPVGEQEIHHTGRSKPDTEGNAVSLVPPDLTENPAGLRG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ASPQHHLFGVYPSRAGNYLRPYPVGEQEIHHTGRSKPDTEGNAVSLVPPDLTENPAGLRG 120

Qy        121 AVEEPAAPWVGDSPIGQSELLGDDDAYLGNQRSKESLGEAGIQKGSAMAATTTTAIFTTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AVEEPAAPWVGDSPIGQSELLGDDDAYLGNQRSKESLGEAGIQKGSAMAATTTTAIFTTL 180

Qy        181 NEPKPETQRRGWAKSRQRRQVWKRRAEDGQGDSGISSHFQPWPKHSLKHGVKKSPPEESN 240
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        181 NEPKPETQRRGWAKSRQRRQVWKRRAEDGQGDSGISSHFQPWPKHSLKHRVKKSPPEESN 240

Qy        241 QNGGEGSYREAETFNSQVGLPILYFSGRRERLLLRPEVLAEIPREAFTVEAWVKPEGGQN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 QNGGEGSYREAETFNSQVGLPILYFSGRRERLLLRPEVLAEIPREAFTVEAWVKPEGGQN 300

Qy        301 NPAIIA------------------------------------------------------ 306
              ||||||
Db        301 NPAIIAGVFDNCSHTVSDKGWALGIRSGKDKGKRDARFFFSLCTDRVKKATILISHSRYQ 360

Qy        307 ------------------------------------------------------------ 306

Db        361 PGTWTHVAATYDGRHMALYVDGTQVASSLDQSGPLNSPFMASCRSLLLGGDSSEDGHYFR 420

Qy        307 ------------------------------------------------------------ 306

Db        421 GHLGTLVFWSTALPQSHFQHSSQHSSEEEEATDLVLTASFEPVNTEWVPFRDEKYPRLEV 480

Qy        307 ------------------------------------------------------------ 306

Db        481 LQGFEPEPEILSPLQPPLCGQTVCDNVELISQYNGYWPLRGEKVIRYQVVNICDDEGLNP 540

Qy        307 ------------------------------------------------------------ 306

Db        541 IVSEEQIRLQHEALNEAFSRYNISWQLSVHQVHNSTLRHRVVLVNCEPSKIGNDHCDPEC 600

Qy        307 ------------------------------------------------------------ 306

Db        601 EHPLTGYDGGDCRLQGRCYSWNRRDGLCHVECNNMLNDFDDGDCCDPQVADVRKTCFDPD 660

Qy        307 ----------------------------------------------------GGIVLSPA 314
                                                                 ||||||||
Db        661 SPKRAYMSVKELKEALQLNSTHFLNIYFASSVREDLAGAATWPWDKDAVTHLGGIVLSPA 720

Qy        315 YYGMPGHTDTMIHEVGHVLGLYHVFKGVSERESCNDPCKETVPSMETGDLCADTAPTPKS 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 YYGMPGHTDTMIHEVGHVLGLYHVFKGVSERESCNDPCKETVPSMETGDLCADTAPTPKS 780

Qy        375 ELCREPEPTSDTCGFTRFPGAPFTNYMSYTDDNCTDNFTPNQVARMHCYLDLVYQQWTES 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ELCREPEPTSDTCGFTRFPGAPFTNYMSYTDDNCTDNFTPNQVARMHCYLDLVYQQWTES 840

Qy        435 RKPTPIPIPPMVIGQTNKSLTIHWLPPISGVVYDRASGSLCGACTEDGTFRQYVHTASSR 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RKPTPIPIPPMVIGQTNKSLTIHWLPPISGVVYDRASGSLCGACTEDGTFRQYVHTASSR 900

Qy        495 RVCDSSGYWTPEEAVGPPDVDQPCEPSLQAWSPEVHLYHMNMTVPCPTEGCSLELLFQHP 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RVCDSSGYWTPEEAVGPPDVDQPCEPSLQAWSPEVHLYHMNMTVPCPTEGCSLELLFQHP 960

Qy        555 VQADTLTLWVTSFFMESSQVLFDTEILLENKESVHLGPLDTFCDIPLTIKLHVDGKVSGV 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 VQADTLTLWVTSFFMESSQVLFDTEILLENKESVHLGPLDTFCDIPLTIKLHVDGKVSGV 1020

Qy        615 KVYTFDERIEIDAALLTSQPHSPLCSGCRPVRYQVLRDPPFASGLPVVVTHSHRKFTDVE 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 KVYTFDERIEIDAALLTSQPHSPLCSGCRPVRYQVLRDPPFASGLPVVVTHSHRKFTDVE 1080

Qy        675 VTPGQMYQYQVLAEAGGELGEASPPLNHIHGAPYCGDGKVSERLGEECDDGDLVSGDGCS 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 VTPGQMYQYQVLAEAGGELGEASPPLNHIHGAPYCGDGKVSERLGEECDDGDLVSGDGCS 1140

Qy        735 KVCELEEGFNCVGEPSLCYMYEGDGICEPFERKTSIVDCGIYTPKGYLDQWATRAYSSHE 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 KVCELEEGFNCVGEPSLCYMYEGDGICEPFERKTSIVDCGIYTPKGYLDQWATRAYSSHE 1200

Qy        795 DKKKCPVSLVTGEPHSLIRTSYHPDLPNHRPLTGWFPCVASENETQDDRSEQPEGSLKKE 854
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1201 DKKKCPVSLVTGEPHSLICTSYHPDLPNHRPLTGWFPCVASENETQDDRSEQPEGSLKKE 1260

Qy        855 DEVWLKVCFNRPGEARAIFIFLTTDGLVPGEHQQPTVTLYLTDVRGSNHSLGTYGLSCQH 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 DEVWLKVCFNRPGEARAIFIFLTTDGLVPGEHQQPTVTLYLTDVRGSNHSLGTYGLSCQH 1320

Qy        915 NPLIINVTHHQNVLFRHTTSVLLNFSSPRVGISAVALRTSSRIGLSAPSNCISEDEGQNH 974
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Db       1321 NPLIINVTHHQNVLFHHTTSVLPNFSSPRVGISAVALRTSSRIGLSAPSNCISEDEGQNH 1380

Qy        975 QGQSCIHRPCGKQDSCPSLLLDHADVVNCTSIGPGLMKCATTCQRGFALQASSEQYIRLM 1034
              |||||||||||||||||||||||||||||||||||||||| |||||||||||| |||| |
Db       1381 QGQSCIHRPCGKQDSCPSLLLDHADVVNCTSIGPGLMKCAITCQRGFALQASSGQYIRPM 1440

Qy       1035 QKEILLTCSSGHWDQNVSCLPVDCGVPDPSLVNYANFSCSEGTKFLKRCSISCVPPAKLQ 1094
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 QKEILLTCSSGHWDQNVSCLPVDCGVPDPSLVNYANFSCSEGTKFLKRCSISCVPPAKLQ 1500

Qy       1095 GLSPWLTCLEDGLWSLPEVYCKLECDAPPIILNANLLLPHCLQDNHDVGTICKYECKPGY 1154
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GLSPWLTCLEDGLWSLPEVYCKLECDAPPIILNANLLLPHCLQDNHDVGTICKYECKPGY 1560

Qy       1155 YVAESAEGKVRNKLLKIQCLEGGIWEQGSCIPVVCEPPPPVFEGMYECTNGFSLDSQCVL 1214
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 YVAESAEGKVRNKLLKIQCLEGGIWEQGSCIPVVCEPPPPVFEGMYECTNGFSLDSQCVL 1620

Qy       1215 NCNQEREKLPILCTKEGLWTQEFKLCENLQGECPPPPSELNSVEYKCEQGYGIGAVCSPL 1274
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 NCNQEREKLPILCTKEGLWTQEFKLCENLQGECPPPPSELNSVEYKCEQGYGIGAVCSPL 1680

Qy       1275 CVIPPSDPVMLPENITADTLEHWMEPVKVQSIVCTGRRQWHPDPVLVHCIQSCEPFQADG 1334
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db       1681 CVIPPSDPVMLPENITADTLEHWMEPVKVQSIVCTGRRQWHPDPVLVHCIQSCEPFQANG 1740

Qy       1335 WCDTINNRAYCHYDGGDCCSSTLSSKKVIPFAADCDLDECTCRDPKAEENQ 1385
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 WCDTINNRAYCHYDGGDCCSSTLSSKKVIPFAADCDLDECTCRDPKAEENQ 1791
```

Search completed: February 3, 2006, 15:11:04
Job time : 3.87272 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 3, 2006, 15:16:21 ; Search time 0.001 Seconds
(without alignments)
1.064 Million cell updates/sec

Title: US-10-675-685-7
Perfect score: 94
Sequence: 1 MMCLKILRISLAILAGWAL 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 56 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : US10675685_2.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	21.3	20	1	US-10-675-685-18	Sequence 18, Appl
2	14	14.9	36	1	US-10-675-685-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-675-685-18
; Sequence 18, Application US/10675685
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 18
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-675-685-18

Query Match 21.3%; Score 20; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy         12 AILAG 16
              ||:||
Db          6 AIIAG 10
```

RESULT 2
US-10-675-685-14
; Sequence 14, Application US/10675685
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 14
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-675-685-14

Query Match 14.9%; Score 14; DB 1; Length 36;
Best Local Similarity 28.6%; Pred. No. 0;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Qy         11 LAILAGW 17
              :|: : |
Db         28 VALPSRW 34
```

Search completed: February 3, 2006, 15:16:22
Job time : 0.001 secs